



SEQUENCE LISTING

<110> Parales, R.
Gibson, D.
Resnick, S.
Lee, K.

<120> Novel naphthalene dioxygenase and methods for their use

<130> 875.006US2

<140> US 09/843,250
<141> 2001-04-26

<150> PCT/US99/25079
<151> 1999-10-26

<150> US 60/105,575
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<223> A sequence encoding an NDO mutant.

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<210> 4
<211> 2515
<212> DNA
<213> Artificial Sequence

<220>
<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

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<210> 5
<211> 9706
<212> DNA
<213> Artificial Sequence

<220>
<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

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<210> 6
<211> 2294
<212> DNA
<213> Artificial Sequence

<220>
<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

<221> misc_feature
<222> (186)...(186)
<223> n = a or t or g or c

<400> 6

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ggtaatntacg	ctaccgacaa	cctgtgcacg	catgttccg	cccgcatgag	tgatggttat	180
ctcgagggta	gagaatcga	atgcccctg	catcaaggc	ggtttgcgt	ttgcacaggc	240
aaagccctgt	gcgcacccgt	gacacagaac	atcaaaacat	atccagtc	gattgagaac	300
ctgcgcgtaa	tgattgattt	gagctaagaa	ttttaacagg	aggcaccccg	ggcccttagag	360
cgtaatcacc	cccatccat	cttttttagg	tgaaaacatg	aattacaata	ataaaatctt	420
ggtaagtcaa	tttggctga	gccaaaagca	cctgattcat	ggcgatgaag	aactttcca	480
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ctgcgttta	ctcgctttat	ccaacgc	caggccgaa	tggacgtaaa	tgacaaagag	2160
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gtcttctacg	ccgc					2280
						2294

<210> 7
<211> 4355
<212> DNA
<213> Artificial Sequence

<220>
<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

<400> 7

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aagccgcgt	accgcgtccg	ccatatgct	gagtgagtgc	gctaaggctg	ggccgcctaa	180
tggcttcgag	aataaagcgg	gccaggtat	ttctctgtca	tctcgccgaa	tgggtggaa	240
cacatcaacc	tgaccggcga	ttacgtctgg	cggtcgatgc	gcagactgga	ggtcgccgaa	300
ttccggccgt	tacggcgcc	ctgaaaacct	tagtgtacga	tttttccgt	tttctctatt	360

cggcctgcgt	tgcgacgttc	gatctgacta	ggggcgcagcg	gcaacatcg	ctgagtacga	420
tccagcgct	ggatctgggt	tatttcgtca	accgacaaca	ccagagcg	tttccgggtgg	480
ttcaggtaaa	gcccaaccac	attgactacc	tctcggcaaa	atgagggtcg	ttactaattt	540
tgaacgtctt	caagcgatgg	ggtttttaggt	cggaagctgc	ccagacctgc	ccaacacctacc	600
acgtcggtac	ccgagcatat	tcggcccg	gcccggaaaaaa	acacagaat	gagcgggtga	660
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aatacatgac	tacttcagac	gattcgtcgat	attcacgtcg	gtgataaaca	aattcaacta	780
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taagccggat	ttatggaact	tctcatacag	ccaaacaatc	gcctcattag	cttttagtccc	900
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ccgccccggga agacaaaatgg aaacgtggcg aagggtggagt gcgaaaattg gtccagcgat	4260
tcgtggatta cccagagcgc atacttcaga cgcacaatct gatggtctt ctgtgatcca	4320
tgaccactt ttacaaaatgg tgactgctac cgccg	4355

<210> 8
<211> 2176
<212> DNA
<213> Artificial Sequence

<220>
<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

<400> 8	
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tcgagggggcg agaaatcgaa tgccccttc atcaaggtcg gtttgcgtt tgtacaggca	180
gagccctctg cgccccctgt acagagaaca tcaaaacata tgcagtcaag attgagaacc	240
tgcgcgtaat gattgattt agctgagaat ttttaatagg aggcgcggcc gaccatagag	300
cgttaattatc cccattccat ctttttttag gtgaaaacat gaattacaaa aacaaaatct	360
tggtaagtga gtctgggctg accccaaaagc acctgattca tggcgtatgaa gaactttcc	420
agcacgaact gagaaccatt tktgcgcqga actgctttt tctcactcat gacagcctga	480
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ggcaaagcga cggttcgatt cgtgccttcc tgaacgtttt ccggcacccgc ggcaagacac	600
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gctgcgcctt actcgcttca tcaccaatgt ccagccgcgatggacgtaa atgatgaaga	2100
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tgtcttctac gcccggcc	2176

<210> 9
<211> 14462
<212> DNA
<213> Artificial Sequence

<220>
<223> A modified DNA molecule encoding valine at the

position corresponding to the F352 amino acid in NDO.

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tgatcgatttccgc ttcaaaataa attcaactat gctttatgtt caaataaaaag	3660
aatcacaaca ttcatgctgg tgataaataa atcaactat tataaaatta agccggattt atgaaaacttc	3720
cacactcacc atcatcgca atacaatct tataaaatta agccggattt atgaaaacttc	3780
tcatacagcc aaacaatcgc ctcattagct ttatcccgg cgccaaacctt ctggaaagtgc	3840
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tcgctattga gtcgcccact cacgatatcc gtcgcctacg cgatgcctc gccaagccct	4140
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<212> DNA

<213> Artificial Sequence

<220>

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<210> 14

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:3.

<400> 14

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Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala			
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Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu			
115	120	125	
Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe			
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His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met			
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 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 15
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:4.

<400> 15
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110

Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 16
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:5.

<400> 16
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60

Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Cys Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 17
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> A polypeptide encoded by SEQ ID NO:6.

<400> 17
Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Phe Gly Leu Ser Gln
1 5 10 15

Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Arg Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 18
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:7.

<400> 18

Met Asn Tyr Lys Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Thr Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Arg
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ser Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Ser Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Asn Ala Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Ile Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ala Ser Leu Ala Gly Asn Ala Val Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ser Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu Asp Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 19
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> A polypeptide encoded by SEQ ID NO:8.

<221> SITE
<222> (35)...(35)
<223> Xaa = any amino acid.

<400> 19
Met Asn Tyr Lys Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Thr Gln
1 5 10 15
Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Arg
20 25 30
Thr Ile Xaa Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
35 40 45
Pro Ser Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
50 55 60
Ile Val Ser Arg Gln Ser Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
65 70 75 80
Cys Arg His Arg Gly Lys Thr Leu Val Asn Ala Glu Ala Gly Asn Ala
85 90 95
Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
100 105 110
Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Glu Ser Leu
115 120 125
Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
130 135 140
His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Ser Leu Met
145 150 155 160
Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Ile Phe Lys His
165 170 175
Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
180 185 190
Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
195 200 205
Val Gly Trp Thr His Ala Ser Ser Leu Arg Thr Gly Glu Ser Ile Phe
210 215 220
Ser Ser Leu Ala Gly Asn Ala Val Leu Pro Pro Glu Gly Ala Gly Leu
225 230 235 240
Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
245 250 255
Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
260 265 270
Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Pro
275 280 285
Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
290 295 300
Ser Val Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
305 310 315 320
Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
325 330 335
Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ala Val Gln Arg Thr Val
340 345 350
Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr
355 360 365
Ala Ser Gln Asn Gly Lys Tyr Gln Ser Arg Asp Ser Asp Leu Ile
370 375 380

Ser Asn Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu Asp Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 20
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:9.

<400> 20
 Met Asn Tyr Lys Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Thr Gln
 1 5 10 15
 Lys His Leu Ile His Gly Gly Glu Leu Phe Gln His Glu Leu Arg
 20 25 30
 Ala Val Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ser Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Ser Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Asn Ala Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Ala Cys Ile Asp Gln Glu Ala Pro Ser Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Ile Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Cys Thr Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Val Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Val Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335

Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ala Val Gln Arg Thr Val
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Ile
 370 375 380
 Ser Asn Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu Asp Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 21
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:10.

<400> 21
 Met Asn Tyr Lys Asn Lys Asn Leu Val Ser Glu Ser Gly Leu Thr Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln Arg Glu Leu Glu
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ser Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Val Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val His Ala Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ala Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Glu Ala Leu
 115 120 125
 Asp Lys Lys Cys Met Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Glu Glu Ala Pro Ser Leu Lys
 145 150 155 160
 Asp Tyr Met Gly Asp Ala Gly Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Ile Gly Pro Pro Gly Lys Val Ile Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Thr Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Gln Ser Val Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Glu Val Arg
 275 280 285

Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Phe Leu Thr Cys Ser Gly Val Phe Lys Val Trp His Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Met Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Val Asp Ala Val Gln Arg Thr Val
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 355 360 365
 Val Ser Gln Asn Ala Lys Lys Tyr Gln Ser Arg Asp Gly Asp Leu Val
 370 375 380
 Ser Asn Leu Gly Phe Gly Asp Val Tyr Gly Asp Glu Val Tyr Pro
 385 390 395 400
 Gly Ile Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gly Ala His Ile Ser Ser Ser Trp Ala Glu Phe
 420 425 430
 Glu Asp Val Ser Lys Asn Trp His Thr Glu Leu Ala Lys Thr Thr Asp
 435 440 445
 Arg

<210> 22
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:11.

<400> 22
 Met Ile Tyr Glu Asn Leu Val Ser Glu Ala Gly Leu Thr Gln Lys His
 1 5 10 15
 Leu Ile His Gly Asp Lys Glu Leu Phe Gln His Glu Leu Lys Thr Ile
 20 25 30
 Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile Pro Ser
 35 40 45
 Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Val Asp Glu Val Ile Val
 50 55 60
 Ser Arg Gln Asn Asp Gly Ser Val Arg Ala Phe Leu Asn Val Cys Arg
 65 70 75 80
 His Arg Gly Lys Thr Leu Val His Ala Glu Ala Gly Asn Ala Lys Gly
 85 90 95
 Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly Glu Leu
 100 105 110
 Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Asp Thr Ile Lys Lys
 115 120 125
 Lys Cys Leu Gly Leu Lys Glu Val Pro Arg Ile Glu Ser Phe His Gly
 130 135 140
 Phe Ile Tyr Gly Cys Phe Asp Ala Glu Ala Pro Thr Leu Val Asp Tyr
 145 150 155 160
 Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Ile Phe Lys His Ser Gly
 165 170 175
 Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys Ala Asn
 180 185 190
 Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His Val Gly
 195 200 205
 Trp Thr His Ala Ser Ser Leu Arg Ser Gly Gln Ser Ile Phe Thr Pro
 210 215 220
 Leu Ala Gly Asn Ala Met Leu Pro Pro Glu Gly Ala Gly Leu Gln Met
 225 230 235 240

Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly Tyr Ser
 245 250 255
 Gly Val His Ser Ala Asp Leu Val Pro Glu Met Met Ala Phe Gly Gly
 260 265 270
 Ala Lys Gln Glu Lys Leu Ala Lys Glu Ile Gly Asp Val Arg Ala Arg
 275 280 285
 Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn Ser Ile
 290 295 300
 Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp Glu Asn
 305 310 315 320
 Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met Pro Glu
 325 330 335
 Asp Leu Lys Arg Arg Leu Ala Asp Ala Val Gln Arg Thr Val Gly Pro
 340 345 350
 Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr Glu Ser
 355 360 365
 Gln Asn Ala Lys Lys Tyr Gln Ser Ser Asn Ser Asp Leu Ile Ala Asn
 370 375 380
 Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Glu Cys Tyr Pro Gly Val
 385 390 395 400
 Val Ala Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe Tyr Arg
 405 410 415
 Ala Tyr Gln Ala His Ile Ser Ser Asn Trp Ala Glu Phe Glu Asn
 420 425 430
 Thr Ser Arg Asn Trp His Thr Glu Leu Thr Lys Thr Thr Asp Arg
 435 440 445

<210> 23
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:12.

<400> 23
 Met Ser Tyr Gln Asn Leu Val Ser Glu Ala Gly Leu Thr Gln Lys Leu
 1 5 10 15
 Leu Ile His Gly Asp Lys Glu Leu Phe Gln His Glu Leu Lys Thr Ile
 20 25 30
 Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile Pro Ser
 35 40 45
 Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Val Asp Glu Val Ile Val
 50 55 60
 Ser Arg Gln Asn Asp Gly Ser Val Arg Ala Phe Leu Asn Val Cys Arg
 65 70 75 80
 His Arg Gly Lys Thr Leu Val His Thr Glu Ala Gly Asn Ala Lys Gly
 85 90 95
 Phe Val Cys Gly Tyr His Gly Trp Gly Tyr Gly Ser Asn Gly Glu Leu
 100 105 110
 Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Asp Ala Ile Lys Lys
 115 120 125
 Lys Cys Leu Gly Leu Lys Glu Val Pro Arg Ile Glu Ser Phe His Gly
 130 135 140
 Phe Ile Tyr Gly Cys Phe Asp Ala Glu Ala Pro Pro Leu Ile Asp Tyr
 145 150 155 160
 Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Thr Phe Lys His Ser Gly
 165 170 175
 Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Val Lys Ala Asn
 180 185 190
 Trp Lys Pro Phe Ala Glu Asn Phe Val Gly Asp Ile Tyr His Val Gly
 195 200 205

Trp Thr His Ala Ala Leu Arg Ala Gly Gln Ser Val Phe Ser Ser
 210 215 220
 Leu Ala Gly Asn Ala Lys Leu Pro Pro Glu Gly Ala Gly Leu Gln Met
 225 230 235 240
 Thr Ser Lys Tyr Gly Ser Gly Met Gly Leu Thr Trp Asp Tyr Tyr Ser
 245 250 255
 Gly Asn Phe Ser Ala Asp Met Val Pro Asp Leu Met Ala Phe Gly Ala
 260 265 270
 Ala Lys Gln Glu Lys Leu Ala Lys Glu Ile Gly Asp Val Arg Ala Arg
 275 280 285
 Ile Tyr Arg Ser Ile Leu Asn Gly Thr Val Phe Pro Asn Asn Ser Phe
 290 295 300
 Leu Thr Gly Ser Ala Thr Phe Lys Val Trp Asn Pro Ile Asp Glu Asn
 305 310 315 320
 Thr Thr Glu Val Trp Thr Tyr Ala Phe Val Glu Lys Asp Met Pro Glu
 325 330 335
 Asp Leu Lys Arg Arg Leu Ala Asp Ala Ala Gln Arg Ser Val Gly Pro
 340 345 350
 Ala Gly Phe Trp Glu Ser Asp Asp Asn Glu Asn Met Glu Thr Leu Ser
 355 360 365
 Gln Asn Ala Lys Lys Tyr Gln Ser Ser Asn Ser Asp Gln Ile Ala Ser
 370 375 380
 Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Glu Cys Tyr Pro Gly Val
 385 390 395 400
 Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe Tyr Arg
 405 410 415
 Ala Tyr Gln Ala His Ile Ser Ser Ser Asn Trp Ala Glu Phe Glu Asn
 420 425 430
 Ala Ser Arg Asn Trp His Thr Glu Leu Thr Lys Thr Thr Asp Arg
 435 440 445

<210> 24

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:13.

<400> 24

Met Arg Gln Ala Ile Met Ser Tyr Gln Asn Leu Val Ser Glu Ala Gly
 1 5 10 15
 Leu Thr Gln Lys His Leu Ile Tyr Gly Asp Lys Glu Leu Phe Gln His
 20 25 30
 Glu Leu Lys Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp
 35 40 45
 Ser Leu Ile Pro Ser Pro Gly Asp Tyr Val Lys Ala Lys Met Gly Val
 50 55 60
 Asp Glu Val Ile Val Ser Arg Gln Asn Asp Gly Ser Val Arg Ala Phe
 65 70 75 80
 Leu Asn Val Cys Arg His Arg Gly Lys Thr Ile Val Asp Ala Glu Ala
 85 90 95
 Gly Asn Ala Lys Gly Phe Val Cys Gly Tyr His Gly Trp Gly Tyr Gly
 100 105 110
 Ser Asn Gly Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly
 115 120 125
 Asp Ala Ile Lys Lys Cys Leu Gly Leu Lys Glu Val Pro Arg Ile
 130 135 140
 Glu Ser Phe His Gly Phe Ile Tyr Gly Cys Phe Asp Ala Glu Ala Pro
 145 150 155 160
 Pro Leu Ile Asp Tyr Leu Gly Asp Val Ala Trp Tyr Leu Glu Pro Thr
 165 170 175

Phe Lys His Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Ala Lys Val
 180 185 190
 Val Val Lys Gly Asn Trp Lys Val Phe Ala Glu Asn Phe Val Gly Asp
 195 200 205
 Ile Tyr His Ile Gly Trp Thr His Ala Ser Ile Leu Arg Ala Gly Gln
 210 215 220
 Ala Ile Phe Ala Pro Leu Ala Gly Asn Ala Met Leu Pro Pro Glu Gly
 225 230 235 240
 Thr Gly Leu Gln Ala Thr Thr Lys Tyr Gly Ser Gly Ile Gly Val Ser
 245 250 255
 Leu Asp Ala Tyr Ser Gly Val Gln Ser Ala Asp Leu Val Pro Glu Met
 260 265 270
 Met Ala Phe Gly Gly Ala Lys Gln Glu Lys Leu Ala Lys Glu Ile Gly
 275 280 285
 Asp Val Arg Ala Arg Ile Tyr Arg Ser Gln Val Asn Gly Thr Val Phe
 290 295 300
 Pro Asn Asn Cys Phe Leu Thr Gly Ala Gly Val Phe Lys Val Phe Asn
 305 310 315 320
 Pro Ile Asp Glu Asn Thr Thr Glu Ala Trp Thr Tyr Ala Ile Val Glu
 325 330 335
 Lys Asp Met Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ala Ala Gln
 340 345 350
 Arg Ser Val Gly Pro Ala Gly Tyr Trp Glu Ser Asp Asp Asn Asp Asn
 355 360 365
 Met Val Leu Ser Gln Asn Ala Lys Lys Tyr Gln Ser Ser Asn Ser Asp
 370 375 380
 Leu Ile Ala Asp Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Glu Cys
 385 390 395 400
 Tyr Pro Gly Val Val Ser Lys Ser Ala Phe Ser Glu Thr Asn His Arg
 405 410 415
 Gly Phe Tyr Arg Ala Tyr Gln Ala His Ile Ser Ser Ser Asn Trp Ala
 420 425 430
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 Thr Asp Arg
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<210> 25

<211> 2265

<212> DNA

<213> Pseudomonas sp.

<400> 25

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<210> 26

<211> 449

<212> PRT

<213> Pseudomonas sp.

<400> 26

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Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val	
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Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly	
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 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
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 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
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 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
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 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
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<210> 27
 <211> 2265
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A sequence encoding an NDO mutant.

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<210> 28

<211> 2265

<212> DNA

<213> Artificial Sequence

<220>

<223> A sequence encoding an NDO mutant.

<400> 28

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<210> 29

<211> 2265

<212> DNA

<213> Artificial Sequence

<220>

<223> A sequence encoding an NDO mutant.

<400> 29

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<210> 30

<211> 2265

<212> DNA

<213> Artificial Sequence

<220>

<223> A sequence encoding an NDO mutant.

<400> 30

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cggtgaggac	gtatacggcg	acgc当地ggct	tccaggcgtc	gtcggcaat	cggcgatcgg	1440	
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ggctgagttc	gagcatgcct	ctagta	gcataactgaa	cttacgaa	ctactgatcg	1560	
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tcagagcg	gttataagct	caatgaa	atgaacg	ttt	acaacgaaaa	tttcagca	1860
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cgcttactc	gcttattcac	caacgtcc	ccgc当地atgg	acgttaatga	caaagagcta	1980	
cttcacatcc	gctccaacgt	cattctgcac	ccggc当地ac	gtggcaatca	gttc当地atgtc	2040	
ttctacgccc	ccccggaa	taatggaaa	cgtggc当地a	gtgggat	aaaattgg	2100	
cagcgattcg	tcgat	taacc	cttca	acaatctgat	gttcttctg	2160	
tgattcagtg	accat	ttta	caatgg	ctgcaacc	ggtcaccatt	2220	
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<210> 31
<211> 2265

<212> DNA

<213> Art:

<223>

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aatcaccccc attccatctt tttagtgta aaacatgaat tacaataata aatcttggt
aagtgaatct ggcttgagcc aaaagcacct gattcatggc gatgaagaac ttttccaaca
tgaactgaaa accatTTTG cgCGGAACTG gCTTTTCTC actcatgata gcctgattcc
tgccccggc gactatgtta ccgcaaaaat ggggattgac gaggtcatcg tctcccgca
gaacgacggt tcgattcgtg ctTTTCTGAA cgtttGCCGG catcgTGGCA agacgctgg
gagcgtgaa gcccggcaatg ccaaaggtt tttttgcagc tatcacggct ggggcttccgg
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ctaacagacg agtcgaccat gatgtcaat attcaagaag acaagcttgt ttccgcccac	1620
gacgccgaag agattttcg tttttcaat tgccacgact ctgcttgca acaagaagcc	1680
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gagcaactgcg tggggcaga ggtgcaat caggcattt caccgcgaact ggcgcagct	1800
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ctgaaagttc gagttgagca tcaactggat ccgcggaaact ggggcaacag cccgaagctg	1920
cgctttactc gctttatcac caacgtccag gccgcattt acgtaaatga caaagagcta	1980
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cagcgattcg tcgattaccc agagcgcata cttagacgc acaatctgt ggtcttctg	2160
tgattcgtt accattttt caaatggtca ctgcacccgc ggtcaccatt aatcaaagg	2220
aatgtacgtg tatggcaat caacaagtgc tttcgataac cggtg	2265

<210> 32

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:27.

<400> 32

Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln	
1 5 10 15	
Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys	
20 25 30	
Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile	
35 40 45	
Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val	
50 55 60	
Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val	
65 70 75 80	
Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala	
85 90 95	
Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly	
100 105 110	
Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu	
115 120 125	
Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe	
130 135 140	
His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met	
145 150 155 160	
Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His	
165 170 175	
Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys	
180 185 190	
Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His	
195 200 205	
Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe	
210 215 220	
Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu	
225 230 235 240	
Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly	
245 250 255	
Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe	
260 265 270	
Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg	
275 280 285	
Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn	
290 295 300	

Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Gly
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 33
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:28.

<400> 33
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255

Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Ala
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 34
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:29.

<400> 34
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205

Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Thr
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 35
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:30.

<400> 35
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160

Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Leu
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 36
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:31.

<400> 36
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110

Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Ile
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 37
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A mutagenic oligonucleotide.

<400> 37
 ttcagcgaac ggtcgccct gc

<210> 38
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>

<223> A tetracycline repair oligonucleotide.

<400> 38

gccgggcctc ttgcggata tcgtcca

27

<210> 39

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> An ampicillin knockout oligonucleotide.

<400> 39

gttgccattg ctgcaggcat cgtggtg

27

<210> 40

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> A mutagenic oligonucleotide.

<400> 40

gaggcacccg cggaagcttt tgtgggagat gca

33

<210> 41

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> A mutagenic oligonucleotide.

<400> 41

gcacccgcgg aacaatttgtt gggagatgca

30

<210> 42

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> A mutagenic oligonucleotide.

<400> 42

ccgcggaaag ctttgtggga g

21

<210> 43

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> A mutagenic oligonucleotide.

<400> 43

ccgcggaaaa gcttgtggga gatg

24

<210> 44

<211> 23

<212> DNA		
<213> Artificial Sequence		
<220>		
<223> A mutagenic oligonucleotide.		
<400> 44		
cgcggaaaac gttgtggag atg		23
<210> 45		
<211> 23		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> A mutagenic oligonucleotide.		
<400> 45		
atattcagg tgcgtatcg cag		23
<210> 46		
<211> 34		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> A mutagenic oligonucleotide.		
<400> 46		
ggacggatat tcagggctcc atagcgcaga ct tg		34
<210> 47		
<211> 33		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> A mutagenic oligonucleotide.		
<400> 47		
gacggatatt caggtAACCA tagcgcagac ttg		33
<210> 48		
<211> 30		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> A mutagenic oligonucleotide.		
<400> 48		
ggtgtttca aagtgcgaa cccgatcgac		30
<210> 49		
<211> 26		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> A mutagenic oligonucleotide.		
<400> 49		

ctgttcagcg aaacttcggg cctgct	26
<210> 50	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> A mutagenic oligonucleotide.	
<400> 50	
ctgttcagcg aaggttcggg cctgct	26
<210> 51	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> A mutagenic oligonucleotide.	
<400> 51	
ctgttcagcg aagtttcggg cctgct	26
<210> 52	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> A mutagenic oligonucleotide.	
<400> 52	
ttcagcgaac gctcgggcct gc	22
<210> 53	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> A mutagenic oligonucleotide.	
<400> 53	
ggcctgctgg cttcgcggaa agcgacgaca	30
<210> 54	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> A mutagenic oligonucleotide.	
<400> 54	
gaaagcgcacg ccaatgacaa t	21
<210> 55	
<211> 30	
<212> DNA	
<213> Artificial Sequence	

<220>
 <223> A mutagenic oligonucleotide.

 <400> 55
 acgacaatga caattggaa acagcttcgc 30

 <210> 56
 <211> 2265
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> A sequence encoding an NDO mutant.

 <400> 56
 gagggtagag aaatcgaatg ccccttgcac caaggcggt ttgacgttg cacaggcaaa 60
 gcccgtgcg caccgtgac acagaacatc aaaacatc cagtcaagat tgagaacctg 120
 cgcgtaatga ttgatttgcg ctaagaattt taacaggagg caccggc cctagagcgt 180
 aatcaccccccc attccatctt ttttaggtga aaacatgaat tacaataata aaatcttgg 240
 aagtgaatct ggtctgagcc aaaagcacct gattcatggc gatgaagaac ttttccaaca 300
 tgaactgaaa accatTTTG cgccgaactg gcttttctc actcatgata gcctgattcc 360
 tgccccccggc gactatgtt ccgcggaaat ggggattgac gaggtcatcg tctccggca 420
 gaacgacggg tcgattcgtg ctTTTCTGAA cgTTTGGCGG catcgtggca agacgctgg 480
 gagcgtggaa gccggcaatg ccaaaggTTTGTGTTGAGC tatcacggct ggggcttcgg 540
 ctccaaacgggtaaactgcaga gcttccatt taaaaaagat ctgtacggcg agtcgctcaa 600
 taaaaaATGT ctggggTTGA aagaagtgcg tcgcgtggag agttccatg gcttcatcta 660
 cgggtgcTTTTC gaccaggagg cccctccctt tatgactat ctgggtgacg ctgcgggtt 720
 cctggAACCT atgttcaagc attccggggg tttagaactg gtccgtcctc caggcaaggt 780
 tgtgtatcaag gccaacttggaa aggccccccg ggaaaacttt gtgggagatg cataccacgt 840
 ggggtggacg caccgtctt cgcttcgtc gggggagtct atttctcgat cgctcgctgg 900
 caatgcggcg ctaccacctg aaggcgcagg ctgcggaaatg acctccaaat acggcagcgg 960
 catgggtgtt ttgtgggacg gatattcagg tgtgcatacg gcagacttgg ttccggaaatt 1020
 gatggcatttgcg gggccgtctt gtttctggaa aaggcgcacg aatgacaata tggaaacaggc 1080
 tcggatttat cgcagccacc tcaactgcac cgTTTCCCG aacaacagca tgctgacctg 1140
 ctcgggttt ttcaaaagtat ggaacccgat cgacgcaaaac accaccggagg tctggaccta 1200
 cgccattgtc gaaaaagaca tgcctgagga tctcaagcgc cgcttggccg actctgttca 1260
 gcaacgtgg gggccgtctt gtttctggaa aaggcgcacg aatgacaata tggaaacaggc 1320
 ttgcggaaatc gcaaaatc atcaatcaag agatagtgat ctgcTTTCAA accttggTTT 1380
 cgggtggacg gtatacggcg acgcggctta tccaggcgat gtcggcaaat cggcgatcgg 1440
 cgagaccagt tatcggtt tctaccgggc ttaccaggca cacgtcagca gctccaactg 1500
 ggctgagttc gagcatgcct ctatgtactg gcatactgaa cttacgaaga ctactgtatcg 1560
 ctaacagacg agtcgaccat gatgatcaat attcaagaag acaagctgg ttccggccac 1620
 gacGCCGAAG agattttcg tttttcaat tgccacgact ctgcTTTCA acaagaagcc 1680
 actacgctgc tgacccagga agcgcattt gttggacattt aggcttaccg tgcttggta 1740
 gagcaactgcg tggggtcaga ggtgcataat caggtcattt cacgcgaact ggcgcagct 1800
 tcagagcgatc gttataagct caatgaaggcc atgaacgttt acaacgaaaa ttccggcaaa 1860
 ctgaaagtgcg ggttgcgatc tcaactggat ccgcggaaact ggggcaacag cccgaagctg 1920
 cgctttactc gctttatcac caacgtccag gccgcaatgg acgtaaatga caaagagcta 1980
 cttcacatcc gctccaaacgt cattctgcac cgggcacgac gtggcaatca ggtcgatgtc 2040
 ttctacgccc cccggaaataaaatggaaa cgtggcgaag gtggagtgacg aaaattggtc 2100
 cagcgattcg tcgattaccc agagcgcata cttcagacgc acaatctgtat ggtctttctg 2160
 tgattcgtg accatTTTA caaatggtc caatggcgc ggtcaccatt aatcaaagg 2220
 aatgtacgtg tatggcaat caacaagtgcg tttcgataac cgggt 2265

<210> 57
 <211> 2265
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> A sequence encoding an NDO mutant.

<400> 57

gagggttagag	aaatcgaatg	ccccttgc	caaggtcg	ttgacgttg	cacaggcaa	60
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cgcgtaatga	ttgatttgag	ctaagaattt	taacaggagg	caccccgccc	cctagagcgt	180
aatcaccccc	attccatctt	tttaggtga	aaacatgaat	tacaataata	aaatcttgg	240
aagtgaatct	ggtctgagcc	aaaagcacct	gattcatggc	gatgaagaac	tttccaaca	300
tgaactgaaa	accattttg	cgcggaaactg	gcttttctc	actcatgata	gcctgattcc	360
tgccccccggc	gactatgtt	ccgcaaaaat	ggggattgac	gaggtcatcg	tctccggca	420
gaacgacggt	tcgattcgt	cttttctgaa	cgttgcgg	catcgtggca	agacgctgg	480
gagcgtggaa	gccggcaatg	ccaaaggtt	tgttgcgc	tatcacgct	ggggcttcgg	540
ctccaacgg	gaactgcaga	gcgttccatt	tgaaaaagat	ctgtacgac	agtcgctcaa	600
taaaaaatgt	ctgggggtt	aagaagtgc	tcgcgtgg	agttccatg	gcttcatcta	660
cggttgc	gaccaggagg	cccctccct	tatgactat	ctgggtgac	ctgcttggta	720
cctggAACCT	atgttcaagc	attccggcgg	tttagaactg	gtcggcctc	caggcaaggt	780
tgtgatcaag	gc当地actg	aggcacc	ggaaaactt	gtgggagatg	cataaccacgt	840
gggttggac	cacgcgtctt	cgcttcg	ggggagatct	atcttctcg	cgctcgctgg	900
caatgcggc	ctaccac	aaggcgcagg	cttgc	ac	acggcagcgg	960
catgggtgt	ttgtggac	gatattcagg	tgtgcata	gcagacttgg	ttccggatt	1020
gatggcattc	ggaggcgc	agcaggaag	gctgacaaa	gaaattggcg	atgttgcgc	1080
tcggatttat	cgcagccacc	tcaactgcac	cg	acaacagca	tgctgac	1140
ctcgggtgtt	ttcaaagtat	ggaacccgat	cgacgca	accac	tctggac	1200
cgccattgtc	aaaaagaca	tgccctgag	tctcaagcgc	cgcttggcc	actctgttca	1260
gc当地acggc	gggcctgct	gcttctgg	aagcgc	aatgacaata	tggaaacagc	1320
ttcgcaaaac	ggcaagaaat	atcaatcaag	agatagt	ctgcttca	accttgg	1380
cggtgaggac	gtatacggc	acgcgg	tccaggc	gtcgg	cg	1440
cgagaccagt	tatgtgg	tctaccggc	ttaccaggc	cacgtcag	gctccaact	1500
ggctgagttc	gagcatgc	ctagactt	gcatactg	cttacgaa	ctactgat	1560
ctaacagac	agtcgaccat	gatgatcaat	attcaagaag	acaagctgt	ttccgccc	1620
gacgccc	agattttcg	tttcttcaat	tgccacgact	ctgcttgc	acaagaagcc	1680
actacgct	tgacc	cagg	agcgcattt	ttggacattc	aggcttacc	1740
gagca	ctgggtc	caga	ggtgcaat	caggcattt	cacgcga	1800
tcagagcgt	gttataag	ct	aatgaa	cttacgaa	ctactgat	1860
ctgaaagttc	gagttgag	caact	ggat	ccgcaaaact	ggggcaac	1920
cgttta	tac	caacgtcc	ggcc	acgtaaatg	caaagagct	1980
ttcacatcc	gttccaa	cattctgc	cg	gcaat	ggtcgat	2040
ttctacg	cccg	ggaa	taatgg	ctg	ggactac	2100
cagcgat	tcgatt	accc	agagcgc	cttca	acaatctg	2160
tgattc	accattt	caa	atgg	ctg	caccatt	2220
aatgtac	tgat	ggca	aa	caac	aaagg	2265

<210> 58

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:56.

<400> 58

Met	Asn	Tyr	Asn	Asn	Lys	Ile	Leu	Val	Ser	Glu	Ser	Gly	Leu	Ser	Gln
1						5			10				15		
Lys	His	Leu	Ile	His	Gly	Asp	Glu	Glu	Leu	Phe	Gln	His	Glu	Leu	Lys
						20			25			30			
Thr	Ile	Phe	Ala	Arg	Asn	Trp	Leu	Phe	Leu	Thr	His	Asp	Ser	Leu	Ile
						35			40			45			
Pro	Ala	Pro	Gly	Asp	Tyr	Val	Thr	Ala	Lys	Met	Gly	Ile	Asp	Glu	Val
						50			55			60			
Ile	Val	Ser	Arg	Gln	Asn	Asp	Gly	Ser	Ile	Arg	Ala	Phe	Leu	Asn	Val
						65			70			75			80
Cys	Arg	His	Arg	Gly	Lys	Thr	Leu	Val	Ser	Val	Glu	Ala	Gly	Asn	Ala
						85			90			95			

Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Trp
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 59
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:57.

<400> 59
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45

Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Tyr
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 60
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A mutagenic oligonucleotide.

<400> 60

gttcagcgaa cgggcgggccc tgctgg	26
<210> 61	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> A mutagenic oligonucleotide.	
<400> 61	
gttcagcgaa cggccgggccc tgctgg	26
<210> 62	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
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<223> A mutagenic oligonucleotide.	
<400> 62	
gttcagcgaa cgaccgggccc tgctgg	26
<210> 63	
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<212> DNA	
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gttcagcgaa cgatcgggccc tgctgg	26
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gttcagcgaa cgtggggggccc tgctgg	26
<210> 65	
<211> 25	
<212> DNA	
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<223> A mutagenic oligonucleotide.	
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ttcagcgaac gtacgggcct gctgg	25